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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/627,206

DATE: 08/14/2000
 TIME: 11:23:33

Input Set : A:\9872C2.seq.txt
 Output Set: N:\CRF3\08142000\I627206.raw

3 <110> APPLICANT: Gross, Jane A.
 4 Xu, Wenfeng
 5 Madden, Karen
 6 Yee, David P.
 8 <120> TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
 10 <130> FILE REFERENCE: 98-75C2
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/627,206
 C--> 12 <141> CURRENT FILING DATE: 2000-07-27
 12 <150> PRIOR APPLICATION NUMBER: 60/115,068
 13 <151> PRIOR FILING DATE: 1999-01-07
 15 <150> PRIOR APPLICATION NUMBER: 60/169,890
 16 <151> PRIOR FILING DATE: 1999-12-09
 18 <150> PRIOR APPLICATION NUMBER: 09/479,856
 19 <151> PRIOR FILING DATE: 2000-01-07
 21 <150> PRIOR APPLICATION NUMBER: 09/569,245
 22 <151> PRIOR FILING DATE: 2000-05-11
 24 <160> NUMBER OF SEQ ID NOS: 60
 26 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1192
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (6)...(746)
 37 <400> SEQUENCE: 1
 38 gagta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg agc cgt gtg 50
 39 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val 15
 40 1 5 10 15
 42 gac cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag 98
 43 Asp Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys 30
 44 20 25 30
 47 ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt 146
 48 Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys 45
 49 35 40 45
 51 gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg 194
 52 Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg 60
 53 50 55 60
 55 agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa 242
 56 Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu 75
 57 65 70 75
 59 gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac 290
 60 Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His 90
 61 80 85 90 95
 63 aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca 338
 64 Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala 110
 65 100 105 110

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67 gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc 386
68 Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala
69 115 120 125
71 gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg 434
72 Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg
73 130 135 140
75 ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg 482
76 Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro
77 145 150 155
79 gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc 530
80 Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser
81 160 165 170 175
83 aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc 578
84 Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys
85 180 185 190
87 agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc 626
88 Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro
89 195 200 205
91 act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag 674
92 Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln
93 210 215 220
95 cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct 722
96 Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro
97 225 230 235
99 gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggaggagg aaaggaggag 776
100 Ala Gln Glu Gly Gly Pro Gly Ala
101 240 245
103 ggagagagat ggagaggagg ggagagagaa agagagggtgg ggagaggggga gagagatatg 836
104 agggagagaga gacagaggag gcagagaggg agagaaacag aggagacaga gaggggagaga 896
105 gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga ggcagagaag 956
106 gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga 1016
107 gaggggacaga gagagataga gcaggaggtc ggggcactct gagtcccagt tcccagtga 1076
108 gctgtaggtc gtcacacct aaccacacgt gcaataaagt cctcgtgcct gctgctcaca 1136
109 gcccccagaga gccctcctc ctggagaata aaacctttgg cagctgccct tcctca 1192
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 247
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 2
117 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
118 1 5 10 15
119 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
120 20 25 30
121 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
122 35 40 45
123 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
124 50 55 60
125 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
126 65 70 75 80

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```

127 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
128                               85          90          95
129 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
130                               100         105         110
131 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val
132                               115         120         125
133 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly
134                               130         135         140
135 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala
136                               145         150         155         160
137 Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr
138                               165         170         175
139 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg
140                               180         185         190
141 Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr
142                               195         200         205
143 Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro
144                               210         215         220
145 Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala
146                               225         230         235         240
147 Gln Glu Gly Gly Pro Gly Ala
148                               245
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 360
152 <212> TYPE: DNA
153 <213> ORGANISM: Homo sapiens
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (1)...(360)
159 <400> SEQUENCE: 3
160 atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg agc cgt gtg gac      48
161 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
162 1 5 10 15
164 cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag ttc      96
165 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
166 20 25 30
168 tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga     144
169 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
170 35 40 45
172 cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc     192
173 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
174 50 55 60
176 cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt     240
177 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
178 65 70 75 80
180 gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga     288
181 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
182 85 90 95
184 ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat     336

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```

185 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
186                               100          105          110          360
188   cag gtg gcc ctg gtc tac agc acg
189   Gln Val Ala Leu Val Tyr Ser Thr
190                               115          120
193 <210> SEQ ID NO: 4
194 <211> LENGTH: 120
195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 4
199 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
200   1                               5          10          15
201   Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
202                               20          25          30
203   Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
204                               35          40          45
205   Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
206                               50          55          60
207   Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
208   65                               70          75          80
209   Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
210                               85          90          95
211   Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
212                               100         105          110
213   Gln Val Ala Leu Val Tyr Ser Thr
214                               115          120
216 <210> SEQ ID NO: 5
217 <211> LENGTH: 1377
218 <212> TYPE: DNA
219 <213> ORGANISM: Homo sapiens
221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (14)...(895)
225 <400> SEQUENCE: 5
226   agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg          49
227   Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
228   1                               5          10
230   agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg          97
231   Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
232                               15          20          25
234   gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg          145
235   Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
236                               30          35          40
238   ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc          193
239   Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
240                               45          50          55          60
242   acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc          241
243   Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
244                               65          70          75

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```

246 aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc 289
247 Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
248      80      85      90
250 tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc 337
251 Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
252      95      100      105
254 agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga 385
255 Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
256      110      115      120
258 gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag 433
259 Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu
260      125      130      135
262 cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt 481
263 His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
264      145      150      155
266 gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529
267 Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
268      160      165      170
270 gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag 577
271 Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
272      175      180      185
274 agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625
275 Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
276      190      195      200
278 ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg 673
279 Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
280      205      210      215
282 agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721
283 Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
284      225      230      235
286 tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769
287 Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
288      240      245      250
290 ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg 817
291 Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
292      255      260      265
294 cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865
295 Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
296      270      275      280
298 cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa 915
299 Pro Ala Gln Glu Gly Gly Pro Gly Ala *
300      285      290
302 ggaggaggga gagagatgga gagaggaggga gagagaaaga gaggtgggga gaggggagag 975
303 agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag 1035
304 ggagagagag acagagggag agagagacag aggggaagag aggcagagag ggaaagaggc 1095
305 agagaaggaa agagacagac agagaaggag agaggcagag agggagagag gcagagaggg 1155
306 agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg 1215
307 gcactctgag tcccagttcc cagtgacgct gtaggtcgct atcacctaac cacacgtgca 1275
308 ataaagtctc cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa 1335

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\9872C2.seq.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12